the sample along the capillary tube 16 at a predetermined time period of, for example once per five seconds. Therefore, the sample can be introduced into the ionization part 21 at a predetermined time period T, while the cleaning fluid is introduced into the ionization part 21 during the remainder of the time period. Typically, the sample may be introduced into the ionization part 21 for one second and subsequently the cleaning fluid is introduced for 4 seconds. These steps may be repeated in cycles.

Page 17, please amend the paragraph beginning at line 3 as follows:

Each sample to be prepared in the sample treatment part 11 has its own individual label number. The sample treatment part 11 links such a label number with the information about a predicted SNP portion, followed by sending to the output prediction part 32. In the output prediction part 32, a predicted pattern of a mass spectrum (i.e., a prediction of the relative intensity distribution of the mass spectrum) is calculated. The results of such a calculation are transmitted to the data analysis part 33. The control part 31 sends out a sampling start signal to the sampling part 15. Simultaneously, the control part 31 sends out the label number to the output analysis part 35 so as to link an output of the detector 28 in the mass spectrometric part 24 with the label number of the sample. The output subjected to the output analysis in the output analysis part 35 is transmitted to the data analysis part 33. Among the predicted mass spectrum patterns sent from the output prediction part 32, a prediction having the highest level of matching score (homology) is defined. Then, the results are sent to the recording part 34 and stored together with the label number on a recording medium.

Page 19, please amend the paragraph beginning at line 19 as follows:

In the equation, $S(i)$ denotes the result of the output-analysis of the sample introduced at i-th, obtained from the output analysis part 35; $I(i)$ denotes an output

from the detector 28 of the mass spectrometric part 24 to the output analysis part 35 with respect to a sample introduced at i-th in the order of samples to be measured; w(n) denotes an attribute that represents a degree of the influence (interference) of a sample introduced at (i - n)th in the order of the samples against a measurement value of the sample introduced at ith, which is obtained by actual measurement. For example, if n = 0, then w(0) =1; and m denotes a predetermined natural number. The above equation means that the influences of the remainder of the measurement sample introduced at (i - m)th in the order of the samples is removed from the output I(i) of the detector 28.

Page 20, please amend the paragraph beginning at line 11 as follows:

A factor w(n) can be defined by measuring that the changes in the ion intensities over time detected by the detector 28. If a sample is once introduced into the flow of a cleaning fluid, then the detector 28 of the mass spectrometric part 24 detects the changes in ion intensities of the sample over time. In this case, the ion intensity steeply rises at first and then gradually decreases over time as the genome DNA sample being absorbed on the inner surface of the capillary tube 16 becomes removed and dispersed therefrom. The w(n) can be determined by measuring a relative ion intensity after the time "T x n" from the time at which the maximum ion intensity is observed. In other words, if the maximum ion intensity is 1 (one), then w(1) is determined from the ion intensity measured at the time after T from the time at which the maximum ion intensity is measured and also the ion intensity measured at the time after 2T is determined from w(2).

Page 21, please amend the paragraphs beginning at lines 4 and 15 as follows:

In the actual measurement, the samples that contain genome DNA are intermittently infused into the capillary tube 16 at predetermined intervals (T). In this

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case, however, the cleaning fluid is circulated in the tube 16. If the time T is more than several minutes, the factor w(1) is so small to be almost negligible. If the time T becomes small, for example in the case of T = 4 seconds, then the factor w(1) becomes considerably large. It means that the contamination of the sample arises. Therefore, the processing such as the one indicated by the equation (1) is required.

Fig. 2 shows charts of mass spectra that illustrate an output I(i) from the detector 28 of the mass spectrometric part 24, and outputs S(i), S(i - 1), and S (i - 2) from the output analysis part 35. In this case, the factor w(n) is input in the output analysis part 35 in advance. In the example shown in the figure, the influences of the sample S(i - 1) measured by the immediately preceding measurement and the influences of the sample S(i -2) measured by the measurement preceding the above measurement remarkably appear on the actual output I (i) from the detector 28. Furthermore, the degrees of these influences are more increased when the sample is subjected to the more recent measurement. Therefore, the measurement value S(i) can be obtained only for the i-th sample by performing a weighting and subtracting I(i-1) and I(i-2) from the output I (1) of the detector 28 of the mass spectrometric part 24. Fig. 3 shows an example of actual data obtained by the genome DNA analysis system of the present invention. Figs. 3A, 3B, and 3C represent the examples of the output results (mass spectra) when the samples with genome DNA of 20 base length, 30 base length, and 40 base length are measured. The horizontal axis of the graph represents the value of mass-to-charge ratio (m/z) obtained by dividing the mass m of ion with the number z of charges, and the vertical axis thereof represents a relative ion intensity.

Page 25, please amend the paragraph beginning at line 16 as follows:

Fig. 4 indicates a typical example showing an ion intensity distribution (a distribution profile of peaks) of a mass spectrum to be measured. A relative ion intensity corresponding to "z" or "m/z" can be predicted while the distribution of ion

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intensities (distribution profile of peaks) as shown in Fig. 4 by a broken line is previously determined. It is possible to perform a data analysis with the predictive information using "m/z" of the detected ion only. The analytic accuracy can be increased as the information of the relative ion intensities is added. It is more effective that the information of the relative ion intensity is considered in addition to the value of m/z when the detected ion peak is extremely weak or genome DNA sample is multiplexed.

Page 33, please amend the paragraph beginning at line 9 as follows:

An analysis system used for the present embodiment may be the system shown in Fig. 1. In this case, however, the sample-treatment part 11 can simultaneously perform the procedures of PCR amplification, extension and the like on the predetermined number (n) of different genome DNA fragments to prepare a sample that contains a mixture of the predetermined number (n) of the different genome DNA fragments with different base lengths. In the sampling part 15, a predetermined volume of the sample which makes up the genome DNA fragments having different base lengths is introduced into the capillary tube 16 at predetermined intervals of T. The mass spectrometric part 24 simultaneously performs the measurement on the predetermined number (n) of the different genome DNA fragments to obtain their mass spectra. Furthermore, the output prediction part 32, the output analysis part 35, and the data analysis part 33 of the control system simultaneously perform the analysis on SNPs of the predetermined number (n) of the different genome DNA fragments.

Page 46, please amend the paragraph beginning at line 18 as follows:

wherein m represents a predetermined natural number; w(n) represents a factor that represents the level of influence of the sample measured at n-th before the measurement of the sample which is measured at i-th.